

ABSTRACT OF THE DISCLOSURE

Multiplex methods for discriminating among *Cannabis sativa* L. plants are disclosed. Eight STR loci have been identified from genomic sequences of *Cannabis sativa* L. plants and primer pairs and cocktails suitable for amplifying the STR by

5 multiplex are disclosed. Polymorphisms at these loci were used to resolve genotypes into distinct groups. Kits are provided for use with multiplex instruments to identify DNA in a plant sample. The typing scheme is useful for the forensic identification of marijuana and for linking a marijuana sample to its plant source.